

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:40 ; Search time 2351.15 Seconds  
(Without alignments)  
161.383 Million cell updates/sec

Title: US-09-851-670-14  
Perfect score: 23  
Sequence: 1 gagacacccgcctctcgcga 23

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htgo\_hum:\*  
31: em\_htgo\_inv:\*  
32: em\_htgo\_rnd:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_other:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.2	61.7	51	6	AX159518	AX159518 Sequence
2	13.2	57.4	36	6	AR026622	AR026622 Sequence
3	13.2	57.4	36	9	S59766	S59766 IGVH-pre-B-
4	13	56.5	34	6	AX007196	AX007196 Sequence
5	13	56.5	34	6	AX007368	AX007368 Sequence
6	13	56.5	51	6	AX160002	AX160002 Sequence
7	13	56.5	52	7	PQBMSSE	M5754 Bacterioph
8	13	56.5	52	7	PQBMSSE	M5754 Bacterioph
9	12.8	55.7	41	6	A93667	A93667 Sequence 3
10	12.8	55.7	50	6	AX158612	AX158612 Sequence
11	12.8	55.7	51	6	AX159517	AX159517 Sequence
12	12.6	54.8	27	6	AR126102	AR126102 Sequence
13	12.6	54.8	27	6	AX117880	AX117880 Sequence
14	12.6	54.8	39	6	AR069156	AR069156 Sequence
15	12.6	54.8	39	6	I49577	I49577 Sequence 26
16	12.6	54.8	51	6	AX158897	AX158897 Sequence
17	12.6	54.8	51	6	AX158898	AX158898 Sequence
18	12.4	53.9	26	6	AX003626	AX003626 Sequence
19	12.4	53.9	33	9	HOMIGABM	L06998 Human Ig re
20	12.4	53.9	44	10	RATM/C134	R02426 Rat fast my
21	12.4	53.9	46	6	A16157	A16157 primer. 10/
22	12.4	53.9	51	6	AX116281	AX116281 Sequence
23	12.4	53.9	51	10	AF005618	AF005618 Mus muscu
24	12.4	53.9	56	9	S77443	S77443 Ig VH-immun
25	12.2	53.0	40	6	AR053641	AR053641 Sequence
26	12.2	53.0	40	6	AR053647	AR053647 Sequence
27	12.2	53.0	44	6	AX034957	AX034957 Sequence
28	12.2	53.0	45	6	AR139753	AR139753 Sequence
29	12.2	52.2	20	6	AR100167	AR100167 Sequence
30	12	52.2	20	6	AR137857	AR137857 Sequence
31	12	52.2	20	6	AR149851	AR149851 Sequence
32	12	52.2	20	6	I77253	I77253 Sequence 17
33	12	52.2	26	6	AR125844	AR125844 Sequence
34	12	52.2	26	6	AR126103	AR126103 Sequence
35	12	52.2	26	6	AR140988	AR140988 Sequence
36	12	52.2	26	6	I47256	I47256 Sequence 18
37	12	52.2	30	6	AR125766	AR125766 Sequence
38	12	52.2	30	6	E27394	E27394 Process for
39	12	52.2	30	6	I47178	I47178 Sequence 10
40	12	52.2	31	6	A17338	A17338 partial int
41	12	52.2	35	6	AR140989	AR140989 Sequence
42	12	52.2	37	6	I34928	I34928 Sequence 14
43	12	52.2	39	6	E11361	E11361 DNA encodin
44	12	52.2	40	6	I86249	I86249 Sequence 3
45	12	52.2	45	6	A28989	A28989 oligo 8 fro

ALIGNMENTS

RESULT	1	LOCUS	AX159518	Sequence	2846	from Patent	W00140521.	PAT	22-JUN-2001
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
FEATURES									
source									

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 51)  
Shinkets, R.A. and Leach, M.  
Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
Patent: WO 0140521-A 2846 07-JUN-2001;  
Curagen Corporation (US)  
Location/Qualifiers  
1..51  
/organism="Homo sapiens"

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misc_feature      /db_xref="taxon:9606"
                  26
                  /note="2 of 2 allelic variants (2845 is other entry)"
Accession number  cg42527623"
BASE COUNT       13 a      17 c      16 g      5 t
ORIGIN
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Query Match	61.7%	Score 14.2;	DB 6;	Length 51;
Best Local Similarity	84.2%;	Pred. No. 6.7e+03;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Oy	3	gaacacccgctctctcgca	21
Db	9	GAACACCAGGCTCTCACA	27

[illegible]

ORGANISM	Unknown.
REFERENCE	Unclassified.
REFERENCE	1 (bases 1 to 30)
AUTHORS	Gorski, D.H. and Walsh, K.
TITLE	Growth arrest homeobox gene
JOURNAL	Patent: US 5856121-A 14 05-JAN-1999.
FEATURES	Location/Qualifiers
Source	1..30

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BASE COUNT      4 a      13 c      8 g      5 t
ORIGIN
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Query Match	57.48;	Score 13.2;	DB 6;	Length 30;
Best Local Similarity	83.38;	Pred. No. 2.2e+04;		
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

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QY      3 gaacacccgcctctctgc 20
          |||||  |||  ||
Db      13 GAACACCCCTCTTGGC 30
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RESULT	3
SS9766/c	
LOCUS	SS9766 36 bp mRNA
DEFINITION	PRI 20-MAR-2000
	IGVH-pre-B-specific immunoglobulin heavy chain variable region
	(CDR3' region, V-D-J rearrangement, clone LE 1-17) [human, bone
	marrow, mRNA Recombinant Partial, 36 nt].
CCDS3630	CCDS3630

KEYWORDS  
VERSION  
ACCESSION  
S59766.1  
GI:385405

SOURCE	human bone marrow.
ORGANISM	Homo sapiens

## REFERENCE AUTHORS

# TITLE

JOURNAL  
MEDLINE  
REMARK

J. Clin. Invest. 91 (4), 1616-1629 (1993)  
93232287  
Genbank staff at the National Library of Medicine created this  
entry [NCBI g11bseq 131828] from the original journal article.  
This sequence comes from Fig. 3.  
Map location: X.

FEATURES	
source	location/qualifiers
1. .36	/organism="Homo sapiens /db_xref="taxon:9606"
gene	1. .36

BASE COUNT	6 a	3 c	15 g	12 t
ORIGIN	/note="pre-B-specific immunoglobulin heavy chain variable region"			

Query Match	57.4%	Score 13.2;	DB 9;	Length 36;
Best Local Similarity	83.3%;	Pred. No. 2.2e+04;		
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

QY 6 caccgcgtctctcgcaa 2  
||| ||||| |  
Db 18 CAACCCTCTCTGCACA 1

RESULT	4				
AX007196					
LOCUS					
AX007196		34 bp	DNA	PAT	06-SEP-2000
DEFINITION		Sequence	36	from Patent	WO0000618.
ACCESSION		U0007106			

VERSION	AA007190
KEYWORDS	AX007196.1 GI:9995062
SOURCE	.
ORGANISM	synthetic construct. synthetic construct artificial sequence.
REFERENCE	1 (bases 1 to 34)

**AUTHORS** Leadlay, P.F., Cortes, J., Staunton, J. and Mearthur, H.A  
**TITLE** Polyketides and their synthesis  
**JOURNAL** Patent: WO 0000618-A 36 06-JAN-2000;

LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);  
BIOTICA TECH LTD (GB); MARTHUR HAMISH ALASTAIR IRVIN (US)

FEATURES  
SOURCE

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

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Query Match	56.5%;	Score 13;	DB 6;	Length 34;
Best Local Similarity	76.2%;	Pred. No. 2.8e+04;		
Matches 16;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	1	gagaacacccgcctctcgcga	21
Db	12	GAGACTCGGATTTCCGCA	32

RESULT	5
AX007368	

LOCUS	34 bp	DNA	PAT	06-SEP-2000
AX007368				
DEFINITION	Sequence	36 from Patent WO0000500.		
ACCION	AX007368			

ACCESSION	AX007368
VERSION	AX007368.1
	GI:9995138

KEYWORDS  
SOURCE  
synthetic construct.

ORGANISM      synthetic construct  
artificial sequence

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (cases 1 to 34)  
Leadlay, P.F., Cortes, J., Staunton, J. and McArthur, H.A.  
Polyketides and their synthesis  
Patent: WO 0005500-A 36 06-JAN-2000;

LEADLAY PETER FRANCIS (GB); CORTES JESUS (GB); STAUNTON JAMES (GB);  
BIOTICA TECH LTD (GB); PFIZER (US); MCARTHUR HAMISH ALASTAIR IRVIN  
(US)

FEATURES  
source 1..34  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

BASE COUNT 7 a 10 c 8 g 9 t  
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 34;  
Best Local Similarity 76.2%; Pred. NO. 2.8e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 gagaacaccgcgtctcgcga 21  
12 GAGAACTCGCGATTTCGCCGA 32

RESULT 6  
AX160002 51 bp DNA PAT 22-JUN-2001  
LOCUS  
DEFINITION Sequence 3330 from Patent WO0140521.  
ACCESSION AX160002  
VERSION AX160002.1 GI:14541333  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 51)  
AUTHORS Shinkets, R.A. and Leach, M.  
TITLE Nucleic acid containing single nucleotide polymorphisms and  
methods of use thereof  
Patent: WO 0140521-A 3330 07-JUN-2001;  
JOURNAL Curagen Corporation (US)  
FEATURES  
source 1..51  
Location/Qualifiers  
misc.feature  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 15 a 13 c 14 g 9 t  
ORIGIN

Query Match 56.5%; Score 13; DB 6; Length 51;  
Best Local Similarity 76.2%; Pred. NO. 2.9e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 gagaacaccgcgtctcgcga 21  
6 GAGAGGCCAGCTTCTCCCA 26

RESULT 7  
POBMS5E 52 bp mRNA PHG 28-APR-1993  
LOCUS  
DEFINITION Bacteriophage Q-beta minus strand RNA, 5' terminus.  
ACCESSION M57754  
VERSION M57754.1 GI:215716  
KEYWORDS  
SOURCE Bacteriophage Q-beta RNA.  
ORGANISM Bacteriophage Q-beta  
Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
Allolevivirus; Allolevivirus subgroup III.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Goodman, H.M., Billeter, M.A., Hindley, J. and Weissmann, C.  
TITLE The nucleotide sequence at the 5'-terminus of the Q-beta RNA minus  
strand  
Proc. Natl. Acad. Sci. U.S.A. 67, 921-928 (1970)  
JOURNAL From EMBL 27 entry POBMS5E; dated 13-FEB-1991.  
COMMENT Location/Qualifiers  
FEATURES

source 1..52  
/organism="Bacteriophage Q-beta"  
/db\_xref="taxon:12009"

BASE COUNT 15 a 11 c 17 g 9 t  
ORIGIN

Query Match 56.5%; Score 13; DB 7; Length 52;  
Best Local Similarity 76.2%; Pred. NO. 2.9e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacaccgcgtctcgcga 22  
21 AGATCCCCCTCTCACTCGTAA 41

RESULT 8  
POBPS3E 52 bp ss-RNA PHG 28-APR-1993  
LOCUS  
DEFINITION Bacteriophage Q-beta plus-strand RNA, 3' terminus.  
ACCESSION M25462  
VERSION M25462.1 GI:215723  
KEYWORDS  
SOURCE Bacteriophage Q-beta RNA.  
ORGANISM Bacteriophage Q-beta  
Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
Allolevivirus; Allolevivirus subgroup III.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Goodman, H.M., Billeter, M.A., Hindley, J. and Weissmann, C.  
TITLE The nucleotide sequence at the 5'-terminus of the Q-beta RNA minus  
strand  
Proc. Natl. Acad. Sci. U.S.A. 67, 921-928 (1970)  
JOURNAL Location/Qualifiers  
FEATURES  
source 1..52  
/organism="Bacteriophage Q-beta"  
/db\_xref="taxon:12009"

BASE COUNT 9 a 17 c 11 g 15 t  
ORIGIN

Query Match 56.5%; Score 13; DB 7; Length 52;  
Best Local Similarity 76.2%; Pred. NO. 2.9e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 agaacaccgcgtctcgcga 22  
32 AGATCCCCCTCTCACTCGTAA 12

RESULT 9  
A93667/C 41 bp DNA PAT 22-JAN-2000  
LOCUS  
DEFINITION Sequence 3 from Patent WO9734144.  
ACCESSION A93667  
VERSION A93667.1 GI:6741855  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS Langer, G. and Troschl, L.  
TITLE METHOD OF DETECTING THE EFFECT OF TEST SUBSTANCES USING HEN  
UROKINASE  
Patent: WO 9734144-A 3 18-SEP-1997;  
JOURNAL SCHERING AG (DE); LANGER GERNOT (DE)  
FEATURES  
source 1..41  
Location/Qualifiers  
BASE COUNT 5 a 14 c 15 g 7 t  
ORIGIN

Query Match	55.7%	Score 12.8	DB 6	length 41
Best Local Similarity	87.5%	Pred. No. 3	7e+04	
Matches 14	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Oy	4	aacaccgcgtctctcg	19	
Db	33	accaccgcgtttctcg	18	

[illegible]

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
I (bases 1 to 50)  
Shinkets, R.A. and Leach, M.  
Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
Patent: WO 0140521-A 1940 07-JUN-2001;  
Curagen Corporation (US)

FEATURES	Location/Qualifiers
source	1. .50

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/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature
25..26

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misc_feature
26      /note="Nucleotide deleted between bases 25 and 26
Accession number cg38034239"

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BASE COUNT	ORIGIN	11 a	13 c	18 g	8 t	/note="2 of 2 allelic variants (1939 is other entry)"

Query Match	55.78;	Score 12.8;	DB 6;	Length 50;
Best Local Similarity	87.58;	Pred. No. 3.8e+04;		
Matches 14;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	gagaacaccgcgtctc	16
Db	28	GAGTACGCCGCTCTC	13

RESULT 11  
AX159517

LOCUS	51 bp	DNA	PAT	22-JUN-2001
DEFINITION	Sequence	2845 from Patent WO0140521.		
ACCESSION				
VERSION				

REVISION	AX159517.1	GI:14540848
VERSION		
ACCESSION	AX159517	

**SOURCE ORGANISM**

REFERENCE  
1. (bases 1 to 51)

AUTHORS	Shimkets, R.A. and Leach, M.
TITLE	Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof  
Patent: WO 0140521-A 2845 07-JUN-2001;  
Curagen Corporation (US)

FEATURES	Location/Qualifiers
source	1. .51

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misc_feature      /organism="Homo sapiens"  
                  /db_xref="taxon:9606"  
                  26
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/note="1 of 2 allelic variants (2846 is other entry)"				
Accession number cg42527623"				
BASE COUNT	13	a	16	c
			17	g
				5
				t

## ORIGIN

Query Match	55.7%	Score 12.8;	DB 6;	Length 51;
Best Local Similarity	87.5%;	Pred. No. 3.8e+04;		
Matches 14;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	3	gaacaccgcgtctctc	18
Db	9	GAACACCAAGTCTCTC	24

RESULT	12		
ARI26102/c			
LOCUS	ARI26102	27 bp	DNA
DEFINITION	Sequence	444 from patent US 6177557	PAT
			16-MAY-2001

ACCESSION	ARI26102
VERSION	ARI26102.1
GI	14112164

NETWORKS  
SOURCE  
ORGANISM

REFERENCE	AUTHORS
Unclassified.	1 (bases 1 to 27)
	Janjic, N., Gold, L.

**TITLE** High affinity ligands of basic fibroblast growth factor and thrombin

JOURNAL	Patent: US 6177557-A 444 23-JAN-2001,
FEATURES	Location/Qualifiers
107	

	source	1 . . 2 /	/organism="unknown"		
BASE COUNT	4 a	3 c	13 g	6 t	1 others
ORIGIN					

Query Match	Score	DB	Length
54.88;	12.6;	6;	27;

Best Local Similarity 69.6%; Pred. No. 4.6e+04;  
Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OY      1  gagaacaccgctctctcgaa 23
          | : | ||||| | | | | |
Db      27  GNAACCAACCGCTGTTCCACA 5
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## RESULT 13

AX117880/c					
LOCUS	AX117880	27 bp	DNA	PAT	11-MAY-2001
DEFINITION	Sequence 3003 from Patent WO0129262.				
Accession					

ACCESSION	AX117880
VERSION	AX117880.1
REVISION	GI:14034831

KEYWORDS	.
SOURCE	synthetic construct.
ORGANISM	synthetic construct

artificial sequence.  
1 (bases 1 to 27)

AUTHORS	Picoult-Newburg, L. and Pohl, M.
TITLE	Genotyping reagents, kits and methods of use thereof
JOURNAL	Patent: WO 0129262-A 3003 26-APR-2001;

Orchid Biosciences, Inc. (US),  
Location/Qualifiers

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source
1. .27
/organism="synthetic construct"
/db_xref="taxon:32630"
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· misc_feature      /note="Primer"
                    1. .27
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	/note="n - C3 linker"			
BASE COUNT	4 a	5 c	6 t	1 others
ORIGIN				

Query Match	54.88;	Score 12.6;	DB 6;	Length 27;
Best Local Similarity	75.08;	Pred. No. 4.6e+04;		
Matches 15; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

OY 2 agaaccgcgtctcgcga 21  
 ||||| |||||  
 Db 23 AACACGAGCTCTCTCCGA 4

RESULT 14  
 AR069156 AR069156 39 bp DNA PAT 18-FEB-2000  
 LOCUS Sequence 26 from patent US 5891442.  
 DEFINITION AR069156  
 ACCESSION AR069156  
 VERSION AR069156.1 GI:7220044  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 39)  
 PAOLETTI, E., TAYLOR, J. and GETTIG, R.  
 TITLE Infectious bursal disease virus recombination poxvirus vaccine  
 JOURNAL Patent: US 5891442-A 26 06-APR-1999;  
 FEATURES  
 source 1..39  
 location/Qualifiers  
 1..39  
 BASE COUNT 10 a 12 c 10 g 7 t  
 ORIGIN

Query Match 54.88; Score 12.6; DB 6; Length 39;  
 Best Local Similarity 78.98; Pred. No. 4.7e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 aacaccgcgtctcgcga 22  
 ||||| ||||| |||||  
 Db 3 AACACGAGCTCTCTCCCA 21

RESULT 15  
 149577 149577 39 bp DNA PAT 07-OCT-1997  
 LOCUS Sequence 26 from patent US 5641490.  
 DEFINITION 149577  
 ACCESSION 149577  
 VERSION 149577.1 GI:2471797  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 39)  
 PAOLETTI, E., TAYLOR, J. and GETTIG, R.  
 TITLE Infectious bursal disease virus recombinant poxvirus vaccine  
 JOURNAL Patent: US 5641490-A 26 24-JUN-1997;  
 FEATURES  
 source 1..39  
 location/Qualifiers  
 1..39  
 BASE COUNT 10 a 12 c 10 g 7 t  
 ORIGIN

Query Match 54.88; Score 12.6; DB 6; Length 39;  
 Best Local Similarity 78.98; Pred. No. 4.7e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 aacaccgcgtctcgcga 22  
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 Db 3 AACACGAGCTCTCTCCCA 21

Search completed: March 9, 2002, 00:48:41  
 Job time: 11122 sec

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